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PROJECT 1 ABSTRACT
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Fusarium head blight or scab is a disease of wheat and barley that can cause reduction both in crop yield and grain quality. Understanding the molecular mechanism of fungal pathogenicity and infection processes in *F. graminearum* is crucial for developing more effective fungicides and disease control strategies. In our previous studies, we have identified two novel virulence factors *ZIF1* and *TLP1*, and characterized five non-ribosomal peptide synthetase (NRPS) genes in *F. graminearum*. The major objective of this proposal is to construct two different yeast two-hybrid libraries and to identify *ZIF1*- and *TLP1*-interacting genes by screening these libraries. Since the *zif1* and *tlp1* deletion mutants are significantly reduced in virulence, genes associated with *ZIF1* and *TLP1* are likely to be important for activating or regulating plant infection processes in *F. graminearum*. Yeast two-hybrid libraries constructed in this project will be made available to the *Fusarium* community. The minor objective of this proposal is to analyze putative NRPS clusters in *F. graminearum*. *F. graminearum* have more NRPS genes than the saprophytic fungus *Neurospora crassa* and hemibiotrophic fungus *Magnaporthe grisea*. Some of these NRPS genes may be responsible for synthesizing phytotoxic or mycotoxic products. We plan to determine the expression pattern of genes closely linked to selected NRPS genes and examine the distribution of their homologs in other fungi. Identifying genes functionally related with NRPSs important for plant infection will be helpful to understand their regulation and evolution. Overall, the proposed research will generate valuable genetic materials for *F. graminearum* studies and be useful to further characterize two novel virulence factors. Results from this study will improve our knowledge about pathogenesis and NRPS genes in *F. graminearum*, and may ultimately lead to the development of novel disease control strategies.